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Clinical presentation of reported lyme disease cases among children from Quebec (Canada) between 2009-2017

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Purpose: In southern Canada, Lyme disease (LD) is an emerging tick-borne disease caused by *Borrelia burgdorferi*. Cases have increased from 144 to 987 between 2009 and 2016. The infection is more frequent in children and older adults probably due to increased exposure to high risk areas during outdoor activities. The aim of this study is to describe the clinical presentation and course of illness among children reported in Monteregie, an emerging area from Quebec province located north of New York state.

Methods & Materials: This is a retrospective cohort study of all cases among children (0-18 years) reported to the Monteregie Public Health Directorate between January 2009 and December 2017. Public health records were reviewed. These records are based on information obtained from treating physician and patient at the time of reporting. Follow-up interviews were conducted with patients (or their parents) to assess outcome for 63 cases reported before December 2016. Variables studied included sociodemographic data, detailed clinical presentation and evolution, laboratory results, hospitalization and exposures.

Results: Eighty-five confirmed, probable or suspected cases were reported. Half occurred in the 0-6 age-group. Erythema migrans was mentioned by 73% of cases but only 53% of all cases were reported at the early localized stage. Neurological symptoms (18%) were as frequent as arthritis (16%). Onset of arthritis occurred more often between October and May (55%) compared to other presentations (10%, $p < 0.001$). The follow-up interview was completed for 43 cases (68%) a mean of 3 years after the onset of the disease. Symptoms disappeared within 6 months after treatment in 38 cases (88%) and lasted between 6 and 12 months in 3 cases (7%). Two cases that initially presented with arthritis were still symptomatic respectively 2 and 4 years after treatment.

Conclusion: Lyme disease is emerging in southern parts of Canada. Younger children are at higher risk and patients can seek advice any month of the year. It is important to include LD in the differential diagnosis of cutaneous, neurological or musculoskeletal symptoms in children exposed to at-risk areas. Early diagnosis and treatment could decrease the occurrence of sequelae.

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Epidemiology of dengue and related entomological and environmental factors - Surat City, Gujarat, India 2011-2016

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Purpose: Surat city observed a rising trend in dengue from 2011 to 2016. Our objectives were to estimate the incidence of dengue in terms of time, place and person, analyze the entomological indices pertaining to *Aedes aegypti* breeding and climatic factors for dengue transmission in the city.

Methods & Materials: We analyzed the surveillance data of vector-borne disease control (VBDC) department from 2011 to 2016. We calculated age, sex and location specific cumulative incidence of dengue. The data was plotted to understand the seasonal distribution of cases. Median House index (HI), Breteau index (BI) and container index (CI) were calculated. Temperature, humidity, rainfall and number of patients were correlated with vector density using spearman correlation coefficient (r_s).

Results: Overall 2446 (11%) of 22101 suspected cases were confirmed positive for dengue as per IgM or NS1 ELISA tests. Incidence increased from 1.5 (2011) to 17.5 (2016) per 100,000 population. Incidence was higher among males. Median age of dengue cases was 20 years (Inter quartile range: 14-28). Five (16%) of 32 VBDC units had incidence above the city average since 2012. Incidence was highest post monsoon. The median HI and BI was <1% and the median CI was < 0.4% throughout the study period. Vector density was significantly correlated with humidity ($r_s = 0.556$), rainfall ($r_s = 0.644$) and number of cases ($r_s = 0.708$). Peak vector density followed peak number of rainy days.

Conclusion: Higher incidence in young males and low house index indicates the probable transmission away from the house. The reasons for high incidence in 5 VBDC units require further micro level evaluation to find out the risk factors. Climate is conducive for vector breeding.

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Novel screening ELISA for sensitive detection of Mayaro virus infected patients

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Purpose: Mayaro virus (MAYV) is an emerging alphavirus circulating in Central/South America. It is transmitted to humans by mosquito bites, causing a febrile illness often with prolonged joint inflammation which resembles other infections with co-circulating arboviruses e.g. Dengue (DENV), Chikungunya (CHIKV) or Oropouche virus (OROV). Serological differentiation from alphavirus infections is complicated by antibodies targeting homologous antigens from related viruses (Semliki Forest virus complex), primarily CHIKV. Still, antibody detection can expand the time for diagnostics of acute MAYV infections beyond the short viraemic period suitable for MAYV RNA detection. Here, serum samples of patients with MAYV or other arboviral infections have been analysed with a novel Anti-Mayaro-virus-ELISA for detection of specific IgM and IgG at the Instituto Evadro Chagas.

Methods & Materials: Serum samples originate from Brazilian patients with clinically and serologically characterized febrile infections drawn between day 11 and 117 post symptom onset. Pre-Characterization included analyses for IgM and haemagglutination inhibition (IH) antibodies against MAYV, CHIKV, DENV, Yellow fever virus (YFV), Zika virus (ZIKV), OROV, Eastern and Western Equine Encephalomyelitis virus (EEEV and WEEV) and flaviviruses in general using in-house MAC ELISA and indirect haemagglutination inhibition assay (IHA).

The first collective encompassed 46 samples, including 25 negative and 21 positive for anti-MAYV IgM and IH antibodies. The second collective (n = 12) consisted of 6 anti-MAYV IH antibody positive and 6 anti-MAYV IH antibody negative samples.

Samples were investigated with the Anti-Mayaro-virus-ELISA (Euroimmun, Germany) IgM (collective 1) and IgG (collective 2).

Results: The Anti-Mayaro-virus-ELISA IgM was 100% sensitive (21/21) and 76% specific (19/25). 6 samples with reactivity in the ELISA had been pre-characterized for CHIKV (n = 5/11) or general flavivirus (n = 1/3) infection.

Testing collective 2, the Anti-Mayaro-virus-ELISA IgG revealed a sensitivity of 100% (6/6) at 50% specificity (3/6). 3 samples with anti-CHIKV IH antibody positive but anti-MAYV IH antibody negative pre-characterization were also reactive in the ELISA.

Conclusion: The novel Anti-Mayaro-virus-ELISA IgM and IgG showed high sensitivity at moderate specificity. This specificity meets the expectations and, in the majority of cases, can be explained by the cross-reactivity with antibodies against related viruses, primarily CHIKV. Thus the ELISA are suitable as screening assays reliably detecting MAYV infected patients.

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21.170

Association of acute febrile illness with Chikungunya infection in Northeastern Thailand

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Purpose: Chikungunya caused by a mosquito-borne virus, chikungunya virus (CHIKV), is an acute febrile illness. This disease nowadays becomes an important health problem since its wide spread and many re-emerged outbreaks in over 60 countries. Among the epidemics area, Thailand has been reported for many previous outbreaks and sporadic cases during the last decade. Since the report of an outbreak of CHIKV infection in 1990s, the study on this neglected disease in Khon Kaen and the northeastern region of Thailand is still limited. Therefore, our study aims to investigate the prevalence of CHIKV infection in human population as well as in circulating Aedes mosquito vectors by both molecular and serological diagnosis.

Methods & Materials: A SYBR green-based real-time PCR targeting non-structural protein 1, which is the most conversed region in this viral genome, was used for the detection of CHIKV in 161 plasma samples obtained from acute febrile illness patients on dengue surveillance from June, 2016 till September, 2017 from 8 hospitals in 4 of 20 provinces in Northeastern Thailand – Khon Kaen, Roi Et, Kalasin and Mahasalakham and in 187 pools of the Aedes mosquitoes collected at the patients' house and 100-meter surroundings. The positive viral RNA was confirmed by sequencing. Anti-CHIKV IgM and IgG antibodies in the plasma samples were determined using commercial enzyme-linked immunosorbent assays.

Results: CHIKV-RNA was found in 8 of 161 (4.9%) plasma samples. Meanwhile, the plasma samples were assessed for a seroprevalence, anti-CHIKV IgM and IgG-specific antibodies were detected in 6/161 (3.7%) and 17/161 (10.6%), respectively. The detection of CHIKV-RNA in 187 mosquito pools was performed, 6 pools (3.2%) were positive with CHIKV non-structural protein 1 gene.

Conclusion: Acute febrile illness in Northeastern Thailand may be caused by CHIKV transmitted by Aedes mosquitos besides other arboviruses. Characterization of an existing genetic diversity should be performed for further surveillance.

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21.171

Correlation between dengue virus serotypes in dengue patients and in mosquitoes at patients' houses and surrounding in Northeastern Thailand

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Purpose: Dengue virus (DENV) is the most important causative agent of arthropod-borne viral disease in the tropical and subtropical regions of the world. DENV is transmitted between human to human via mosquitoes, Aedes aegypti and Aedes albopictus. By the late 2000s, the dengue was widespread among regions in Thailand and dengue hemorrhagic fever (DHF) had become a leading cause of hospitalization and death. Meanwhile dengue surveillance by mosquitoes control has been performed immediately after case report. To understand the role of dengue surveillance in Northeastern Thailand, DENV serotypes were investigated in mosquitoes at patients' houses and surrounding area during 2016-2018.

Methods & Materials: One hundred and eighty-eight mosquito pooled samples were collected from 97 dengue fever-suspected patients' houses in 4 provinces in Northeastern Thailand – Khon Kaen, Roi Et, Kalasin and Mahasalakham province. DENV and serotyping were investigated in all pooled mosquito samples by two step reverse transcription quantitative polymerase chain reaction (RT-qPCR) using 5 sets of primer. The plasma samples of dengue fever-suspected patients from 8 hospitals were determined for DENV serotype by RT-PCR

Results: DENV-RNA was found in 28.87% (28/97) of dengue-suspected patients and consisted of DENV-1 (15%), DENV-2 (7%), DENV-3 (17%), and DENV-4 (61%15). Meanwhile, DENV-RNA was found in 34.04% (64/188) of mosquito pools and consisted of DENV-1 (43%), DENV-4 (33%), DENV-2 (16%) and DENV-3 (8%). Interestingly, DENV detection in mosquito pools was positive in both of dengue patients' houses (71%) and DENV negative patients' houses (93%). The matching of DENV serotype in dengue patients and mosquito pools collected from their houses and surrounding area were 57% whereas unmatching DENV serotype was found in 43% of dengue patients and mosquito pools. Most of these patients were students (70%) and workers (29%) who spend day time outside their houses.

Conclusion: The circulation of DENV was found in mosquitoes at patients' houses and surrounding area and also from DENV negative patients' houses. From the correlation of matching DENV serotype result might suggest that the source of DENV transmission is not only from mosquitoes in patient's house but also from others regions.

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